

(FILE 'HOME' ENTERED AT 13:42:14 ON 27 FEB 2001)

INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCCommerce, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL, ...' ENTERED AT 13:42:21 ON 27

FEB

2001

SEA (DS4152) (20W)ANGIO? AND (CANCER OR TUMOR OR TUMOUR)

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1 FILE CANCERLIT

1 FILE CAPLUS

1 FILE IFIPAT

11 FILE USPATFULL

L1

QUE (DS4152) (20W) ANGIO? AND (CANCER OR TUMOR OR TUMOUR)

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FILE 'USPATFULL, CANCERLIT, CAPLUS, IFIPAT' ENTERED AT 13:44:38 ON 27

FEB

2001

L2

14 S (DS4152) (20W)ANGIO? AND (CANCER OR TUMOR OR TUMOUR)

L3

13 DUP REM L2 (1 DUPLICATE REMOVED)

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(FILE 'HOME' ENTERED AT 13:42:14 ON 27 FEB 2001)

INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS,  
BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT,  
CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE,  
DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL, ...' ENTERED AT 13:42:21 ON 27

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SEA (DS4152) (20W) ANGIO? AND (CANCER OR TUMOR OR TUMOUR)

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FILE 'USPATFULL, CANCERLIT, CAPLUS, IFIPAT' ENTERED AT 13:44:38 ON 27

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L2

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13 DUP REM L2 (1 DUPLICATE REMOVED)

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Terms	Documents
15 and example	1

Database:

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IBM Technical Disclosure Bulletins

Refine Search:

15 and example

[Clear](#)**Search History**

Today's Date: 2/27/2001

<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
USPT	15 and example	1	<u>L6</u>
USPT	13 and antibod?	1	<u>L5</u>
USPT	13 and antibody	1	<u>L4</u>
USPT	5912324	1	<u>L3</u>
EPAB	9514714	1	<u>L2</u>
EPAB	9812226	1	<u>L1</u>

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 27, 2001, 08:59:59 ; Search time 15.59 Seconds  
(without alignments)  
19.740 Million cell updates/sec

Title: US-09-307-223-1

Perfect score: 57  
Sequence: 1 CRRETAWAC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 segs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_36.\*  
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
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9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
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13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	9	16	Alpha5/betal integ
2	57	100.0	9	19	RGD-containing pep
3	57	100.0	9	20	Integrin-binding p
4	57	100.0	9	21	Integrin alpha5bet
5	57	100.0	12	20	Integrin-specific
6	57	100.0	12	20	Integrin-specific
7	57	100.0	13	16	Integrin-binding p
8	57	100.0	13	19	Chimeric adenoviru
9	57	100.0	25	20	Integrin-binding p
10	43	75.4	9	16	Alpha5/betal integ
11	43	75.4	10	16	Alpha5/betal integ
12	40	70.2	9	16	Alpha5/betal integ

13	40	70.2	170	20	Y29195	Amino acid sequenc
14	39	68.4	7	16	R76198	Alpha5/betal integ
15	39	68.4	7	16	R76192	Alpha5/betal integ
16	38	66.7	14	20	Y42754	Wheat amyloplast A
17	38	66.7	14	20	Y39332	ADP glucose transp
18	38	66.7	132	20	Y73857	Human prostate tum
19	37	64.9	9	19	W66171	MSH-receptor subty
20	37	64.9	269	21	Y75616	Neisseria meningit
21	37	64.9	269	21	Y75617	Neisseria meningit
22	36	63.2	203	20	Y04837	Mycobacterium spec
23	36	63.2	241	20	Y41528	Fragment of human
24	36	63.2	506	20	Y04841	Mycobacterium spec
25	35	61.4	188	21	Y76166	Human secreted pro
26	35	61.4	230	20	Y36783	Protein which is s
27	35	61.4	237	20	W88124	Primate DCMPI C-le
28	35	61.4	392	11	R07130	H20B receptor. R
29	35	61.4	392	18	W18668	Polliovirus recepto
30	35	61.4	416	11	R07131	H20A receptor. R
31	35	61.4	417	18	W18669	Polliovirus recepto
32	34	59.6	45	20	Y45281	Human secreted pro
33	34	59.6	134	20	Y73896	Human prostate tum
34	34	59.6	357	14	R33560	Antigen produced b
35	34	59.6	384	20	Y42383	Amino acid sequenc
36	34	59.6	384	21	Y84437	Amino acid sequenc
37	34	59.6	444	21	Y76041	Rat skin cell prot
38	34	59.6	444	21	Y76120	Rat skin cell prot
39	34	59.6	659	20	Y06996	Sequence of C3Vs.
40	33	57.9	9	19	W66174	MSH-receptor subty
41	33	57.9	60	20	W88911	Polypeptide fragme
42	33	57.9	211	20	Y31151	Human XPC protein
43	33	57.9	268	13	R28147	Sugar beet chitina
44	33	57.9	271	21	Y74326	Neisseria gonorrhoe
45	33	57.9	437	20	Y32502	Human parkin gene

#### ALIGNMENTS

RESULT 1

ID R76196 standard; peptide; 9 AA.

XX R76196;

AC R76196;

DT 24-JAN-1996 (first entry)

XX Alpha5/betal integrin binding peptide #7.

DE High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;

XX High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;

KW alphav/beta3; RGD; stable configuration; wound healing;

KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;

XX smooth muscle cell migration.

OS Synthetic.

XX W09514714-A1.

XX 01-JUN-1995.

XX 22-NOV-1994; 94WO-US13542.

XX 04-AUG-1994; 94US-0286861.

XX 24-NOV-1993; 93US-0158001.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Koivunen E, Ruoslahti E;

XX WPI; 1995-206899/27.

XX High affinity integrin binding peptides - can be used to attach

PT cells to a substrate, inhibit the attachment of osteoclasts to bone,

PT promote wound healing, inhibit angiogenesis, metastasis of tumours

and migration of smooth muscle cells

Claim 6; Page 60; 86pp; English.

The sequences given in R76185-200 and R79073-94 are high affinity integrin binding peptides which bind to various integrins. Peptides which bind to alpha5/beta1 integrins contain the motifs given in R76185-86 and peptides which bind to alpha5/beta3 and alpha5/beta3 integrins contain the motif given in R76187. Alpha5/beta5 integrins are also bound by RGD containing peptides. These peptides assume a conformationally stabilised configuration which is due to the formation of a disulphide bond, a peptide bond or a lactam bond. These peptides may be used for isolating the complementary integrin from a sample mixture by contacting them under ionic conditions to allow binding of the integrin to the peptide and then separating the integrin from the peptide. They can be used for attaching cells to a substrate, by binding them to the substrate with the cell. The peptides promote wound healing when applied locally and inhibit the attachment of osteoclasts to bone. They inhibit angiogenesis, metastasis of tumours and migration of smooth muscle cells.

Sequence 9 AA;

Query Match 100.0%; Score 57; DB 16; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
DB 1 crretawac 9

RESULT 2  
W57200  
ID W57200 standard; peptide; 9 AA.

AC W57200;  
XX 05-AUG-1998 (first entry)

XX RGD-containing peptide SEQ ID NO:18 from WO9812226 Example 9.

DE Fibronectin; superfibronectin; first type III repeat unit; IIII;  
KW angiogenesis; psoriasis; rheumatoid arthritis; cancer; tumour.

OS Synthetic.  
XX WO9812226-A1.  
XX 26-MAR-1998.

XX 12-SEP-1997; 97WO-US16344.

XX 20-SEP-1996; 96US-0717169.

XX (BURN-) BURNHAM INST.

XX Pasqualini R, Ruoslahti E;

XX WPI; 1998-217210/19.

XX Inhibition of angiogenesis by superfibronectin - useful for  
PT treating, e.g. psoriasis, rheumatoid arthritis and various cancers

XX Example 9; Page 63; 103pp; English.

XX A method has been developed of ameliorating cancer, or inhibiting  
CC angiogenesis, in a subject. The method comprises administering a  
CC superfibronectin or a superfibronectin-generating compound. The  
CC present sequence represents a peptide used in an example of the  
CC present invention. The method can be used to treat cancer, ocular  
CC neovascularisation, diabetic retinopathy, haemangioma, rheumatoid

CC arthritis, psoriasis, granuloma, and granulation tissue. The cancer  
CC treated by the method can comprise a solid tumour, such as a melanoma,  
CC osteosarcoma, ovarian, vascular or epithelial cell tumour. When it is in  
CC an epithelial cell tumour, it is preferably a colon carcinoma, breast  
CC carcinoma, or ovarian carcinoma. When it is a vascular cell tumour, it is  
CC selected from haemangiomas, Kaposi's sarcoma, lymphangioma, glomangioma,  
CC angiosarcoma, or haemangioendothelioma. The method inhibits or prevents  
CC a tumour cell metastasis in a subject especially inhibits the tumour  
CC cell migration, attachment, or inhibiting growth of a tumour cell in a  
CC subject having a pathology with an angioproliferative component, where  
CC the inhibition causes regression of the pathology. The route of  
CC administration is intravenous, intramuscular, intradermal, subcutaneous,  
CC intracranial, intracerebrospinal, epidural, topical or oral  
CC administration.

Sequence 9 AA;

Query Match 100.0%; Score 57; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
DB 1 crretawac 9

RESULT 3  
W95413  
ID W95413 standard; peptide; 9 AA.

XX W95413;

XX 18-MAR-1999 (first entry)

XX Integrin-binding peptide 7.

XX Integrin; transfection complex; integrin-binding; lipid; immunisation;  
KW antisense therapy; enzyme; therapeutic agent; immunogen; cystic fibrosis;  
KW cancer; viral infection; human immunodeficiency virus; cardiovascular;  
KW restenosis; leukaemia; asthma; glaucoma; cyclic; circular.

OS Synthetic.

XX Key Location/Qualifiers  
FH Disulfide-bond 1..9 /note= "disulphide bridge"

XX WO9854347-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-GB01577.

XX 29-MAY-1997; 97GB-0011115.

XX (CHIL-) INST CHILD HEALTH.

XX Hart SL;

XX WPI; 1999-045366/04.

XX New integrin-targeting transfection complex including lipid - used  
PT to improve transfection efficiency for a very wide range of cells,  
PT useful in, e.g. antisense therapy and genetic immunisation

XX Claim 10; Page 50; 70pp; English.

XX The invention relates to an integrin-targeting transfection complex. The  
CC complex comprises a nucleic acid, an integrin-binding component, a  
CC polycationic nucleic acid-binding component and a lipid. The complexes  
CC are used for in vivo or in vitro transfection of cells, specifically:  
CC (i) for treatment or prevention of disease (in humans or other animals)

CC caused by defective or deficient genes; (ii) for immunisation; (iii) for  
 CC antisense therapy, and (iv) for protein production in host cells, e.g.  
 CC of enzymes, therapeutic agents, vaccinating immunogens and diagnostic  
 CC antigens. Typical of the diseases that can be treated or prevented are  
 CC cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency  
 CC virus), cardiovascular disease (e.g. restenosis), leukaemia, asthma and  
 CC glaucoma. Incorporation of the lipid into the complex increases  
 CC transfection levels from 1-10 percent to over 50 percent. This effect is  
 CC observed with all cell types tested including those that are resistant to  
 CC transfection by most plasmid vectors. The complexes can carry large  
 CC genes, up to 125 kb, e.g. an artificial chromosome. The present sequence  
 CC represents a claimed example of an integrin-binding peptide used in the  
 CC transfection complexes.

XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 57; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9  
 |||||  
 Db 1 crretawac 9

RESULT 4

ID Y56389 standard; peptide; 9 AA.

XX Y56389;

DT 16-FEB-2000 (first entry)

DE Integrin alpha5beta1 cyclic peptide antagonist.

XX Integrin alpha5beta1; inhibition; antagonist; cyclic; detection;  
 KW fibronectin; vitronectin; angiogenesis; cancer; anticancer; diagnosis;  
 KW antiporiatic; anti-arthritis; anti-angiogenic; anti-inflammatory;  
 KW anglogenic diseases; diabetic retinopathy; macular degeneration;  
 KW haemangioma; psoriasis; rheumatoid arthritis; osteoarthritis; neoplasm;  
 KW carcinoma; sarcoma; mesothelioma; teratocarcinoma; astrocytoma;  
 KW glioblastoma; metastasis; Crohn's disease; ulcerative colitis.

XX Synthetic.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Disulfide-bond 1..9

PN W09958139-A2.

XX 18-NOV-1999.

PF 07-MAY-1999; 99WO-US09972.

PR 08-MAY-1998; 98US-0084850.

XX (REGC ) UNIV CALIFORNIA.

PI Varner JA;

XX WPI; 2000-038958/03.

XX Reducing or inhibiting angiogenesis in tissue by treatment with an  
 PT agent that interferes with binding of alpha5beta1 integrin with its  
 PT ligand, e.g. for treating cancer

XX Claim 14; Page 55; 68pp; English.

XX The present invention describes a method for reducing or inhibiting  
 CC angiogenesis in a tissue by treating alpha5beta1 integrin (I) in the  
 CC tissue with an agent (II) that interferes with specific binding of (I)

CC to its ligand (III), expressed in the tissue. The present sequence  
 CC represents a specifically claimed (I) cyclic peptide antagonist, for  
 CC use in the method of the invention. (II) are specifically used to treat  
 CC (or, when labeled, to diagnose) angiogenic diseases of the eye (diabetic  
 CC retinopathy or macular degeneration); skin (haemangioma or psoriasis);  
 CC joints (rheumatoid arthritis and osteoarthritis); neoplasms (particularly  
 CC carcinoma, e.g. of breast, colon, ovary and prostate; also sarcoma,  
 CC mesothelioma, teratocarcinoma, astrocytoma and glioblastoma or  
 CC metastatic malignancies); or diseases of bone and intestines (Crohn's  
 CC disease or ulcerative colitis).

XX Sequence 9 AA;

Query Match 100.0%; Score 57; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9

Db 1 crretawac 9

RESULT 5

ID W95412 standard; peptide; 12 AA.

XX W95412;

XX 18-MAR-1999 (first entry)

DE Integrin-specific peptide.

XX Integrin; transfection complex; integrin-binding; lipid; immunisation;  
 KW antisense therapy, enzyme; therapeutic agent; immunogen; cystic fibrosis;  
 KW cancer; viral infection; human immunodeficiency virus; cardiovascular;  
 KW restenosis; leukaemia; asthma; glaucoma.

XX Synthetic.

XX W09854347-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-GB01577.

XX 29-MAY-1997; 97GB-0011115.

XX (CHIL-) INST CHILD HEALTH.

XX Hart SL;

XX WPI; 1999-045366/04.

XX New integrin-targeting transfection complex including lipid - used  
 PT to improve transfection efficiency for a very wide range of cells,  
 PT useful in, e.g. antisense therapy and genetic immunisation

XX Claim 11; Page 50; 70pp; English.

XX The invention relates to an integrin-targeting transfection complex. The  
 CC complex comprises a nucleic acid, an integrin-binding component, a  
 CC polycationic nucleic acid-binding component and a lipid. The complexes  
 CC are used for in vivo or in vitro transfection of cells, specifically:  
 CC (i) for treatment or prevention of disease (in humans or other animals)  
 CC caused by defective or deficient genes; (ii) for immunisation; (iii) for  
 CC antisense therapy, and (iv) for protein production in host cells, e.g.  
 CC of enzymes, therapeutic agents, vaccinating immunogens and diagnostic  
 CC antigens. Typical of the diseases that can be treated or prevented are  
 CC cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency  
 CC virus), cardiovascular disease (e.g. restenosis), leukaemia, asthma and  
 CC glaucoma. Incorporation of the lipid into the complex increases  
 CC transfection levels from 1-10 percent to over 50 percent. This effect is

CC observed with all cell types tested including those that are resistant to  
 CC transfection by most plasmid vectors. The complexes can carry large  
 CC genes, up to 125 kb, e.g. an artificial chromosome. The present sequence  
 CC represents a claimed example of an integrin-binding peptide used in the  
 CC transfection complexes.

XX  
 SQ Sequence 12 AA;

Query Match 100.0%; Score 57; DB 20; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.0031;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
 |||||  
 Db 3 crretawac 11

RESULT 6

ID W95411 standard; peptide; 12 AA.

XX AC W95411;

DT 18-MAR-1999 (first entry)

XX DE Integrin-specific peptide.

XX KW Integrin; transfection complex; integrin-binding; lipid; immunisation;  
 KW antisense therapy; enzyme; therapeutic agent; immunogen; cystic fibrosis;  
 KW cancer; viral infection; human immunodeficiency virus; cardiovascular;  
 KW restenosis; leukaemia; asthma; glaucoma; cyclic; circular.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 3..11 /note= "disulphide bridge"

XX PN WO9854347-A1.

XX PD 03-DEC-1998.

XX PF 29-MAY-1998; 98WO-GB01577.

XX PR 29-MAY-1997; 97GB-0011115.

XX PA (CHIL-) INST CHILD HEALTH.

XX PI Hart SL;

XX DR WPI; 1999-045366/04.

XX New integrin-targeting transfection complex including lipid - used  
 PT to improve transfection efficiency for a very wide range of cells,  
 PT useful in, e.g. antisense therapy and genetic immunisation

XX PS Claim 11; Page 50; 70pp; English.

XX The invention relates to an integrin-targeting transfection complex. The  
 CC complex comprises a nucleic acid, an integrin-binding component, a  
 CC polycationic nucleic acid-binding component and a lipid. The complexes  
 CC are used for in vivo or in vitro transfection of cells, specifically:  
 CC (i) for treatment or prevention of disease (in humans or other animals)  
 CC caused by defective or deficient genes; (ii) for immunisation; (iii) for  
 CC antisense therapy, and (iv) for protein production in host cells, e.g.  
 CC of enzymes, therapeutic agents, vaccinating immunogens and diagnostic  
 CC antigens. Typical of the diseases that can be treated or prevented are  
 CC cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency  
 CC virus), cardiovascular disease (e.g. restenosis), leukaemia, asthma and  
 CC glaucoma. Incorporation of the lipid into the complex increases  
 CC transfection levels from 1-10 percent to over 50 percent. This effect is  
 CC observed with all cell types tested including those that are resistant to

CC transfection by most plasmid vectors. The complexes can carry large  
 CC genes, up to 125 kb, e.g. an artificial chromosome. The present sequence  
 CC represents a claimed example of an integrin-binding peptide used in the  
 CC transfection complexes.

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 57; DB 20; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.0031;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
 |||||  
 Db 3 crretawac 11

RESULT 7

ID R76190 standard; peptide; 13 AA.

XX AC R76190;

DT 24-JAN-1996 (first entry)

XX DE Integrin binding peptide #2.

XX KW High affinity; integrin binding peptide; alpha5/beta1; alpha/beta5;  
 KW alpha/beta3; RGD; stable configuration; wound healing;  
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;  
 KW smooth muscle cell migration.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 3..11

XX PN WO9514714-A1.

XX PD 01-JUN-1995.

XX PF 22-NOV-1994; 94WO-US13542.

XX PR 04-AUG-1994; 94US-0286861.

XX PR 24-NOV-1993; 93US-0158001.

XX PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX PI Koivunen E, Ruoslahti E;

XX DR WPI; 1995-206899/27.

XX High affinity integrin binding peptides - can be used to attach  
 PT cells to a substrate, inhibit the attachment of osteoclasts to bone,  
 PT promote wound healing, inhibit angiogenesis, metastasis of tumours  
 PT and migration of smooth muscle cells

XX PS Example 1; Page 24; 86pp; English.

XX The sequences given in R76185-200 and R79073-94 are high affinity  
 CC integrin binding peptides which bind to various integrins. Peptides  
 CC which bind to alpha5/beta1 integrins contain the motifs given in  
 CC R76185-86 and peptides which bind to alpha/beta5 and alpha/beta3  
 CC integrins contain the motif given in R76187. Alpha/beta5 integrins  
 CC are also bound by RGD containing peptides. These peptides assume a  
 CC conformationally stabilised configuration which is due to the  
 CC formation of a disulphide bond, a peptide bond or a lactam bond.  
 CC These peptides may be used for isolating the complementary integrin  
 CC from a sample mixture by contacting them under ionic conditions to  
 CC allow binding of the integrin to the peptide and then separating the  
 CC integrin from the peptide. They can be used for attaching cells to  
 CC a substrate, by binding them to the substrate with the cell. The  
 CC peptides promote wound healing when applied locally and inhibit the

CC attachment of osteoclasts to bone. They inhibit angiogenesis,  
CC metastasis of tumours and migration of smooth muscle cells.

SQ Sequence 13 AA;

Query Match 100.0%; Score 57; DB 16; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
| | | | | | | | |  
Db 3 crretawac 11

RESULT 8

ID W56041 standard; peptide; 13 AA.

AC W56041;

DT 29-JUL-1998 (first entry)

DE Chimeric adenovirus fiber protein non-native amino acid sequence 35.

XX Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;  
KW constrained peptide motif; gene therapy; cancer; heart disease;  
KW autoimmune disorder.

XX Synthetic.

OS Mastadenovirus.

XX W09807865-A1.

XX 26-FEB-1998.

XX 21-AUG-1997; 97WO-US14719.

XX 21-AUG-1996; 96US-0701124.

XX (GENV.) GENVEC INC.

XX Kovessdi I, Roelvink PW, Wickham TJ;

XX WPI; 1998-169169/15.

XX N-PSDB; V28551.

XX Chimeric adenovirus fibre proteins - containing non-native amino  
PT acid sequence to provide for binding and entry into cells,  
PT especially for gene therapy

PS Claim 7; Page 78; 124pp; English.

XX The present sequence represents a specifically claimed non-native amino  
CC acid sequence from a chimeric adenovirus fibre protein (Afp) of the  
CC present invention. The non-native amino acid sequence allows the  
CC chimeric fibre (or a vector comprising the chimeric fibre) to more  
CC efficiently bind to and enter cells. The products can be used for gene  
CC therapy, for treating cancer, e.g. melanoma, glioma and lung cancers as  
CC well as genetic disorders, e.g. cystic fibrosis, haemophilia and  
CC muscular dystrophy as well as pathogenic infections, e.g. HIV,  
CC tuberculosis and hepatitis and also for heart disease, to e.g. prevent  
CC restenosis following angioplasty or to promote angiogenesis to reperfuse  
CC necrotic tissue, and in autoimmune disorders, e.g. Crohn's disease,  
CC colitis, rheumatoid arthritis, and Alzheimer's disease.

XX Sequence 13 AA;

Query Match

Best Local Similarity 100.0%; Score 57; DB 19; Length 13;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
| | | | | | | | |  
Db 3 crretawac 11

RESULT 9

ID W95416 standard; peptide; 25 AA.

AC W95416;

DT 18-MAR-1999 (first entry)

DE Integrin-binding peptide.

XX Integrin; transfection complex; integrin-binding; lipid; immunisation;  
KW antisense therapy; enzyme; therapeutic agent; immunogen; cystic fibrosis;  
KW cancer; viral infection; human immunodeficiency virus; cardiovascular;  
KW restenosis; leukaemia; asthma; glaucoma; cyclic; circular.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 3..11 /note= "disulphide bridge"

XX W09854347-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-GB01577.

XX 29-MAY-1997; 97GB-0011115.

XX (CHIL-) INST CHILD HEALTH.

XX Hart SL;

XX WPI; 1999-045366/04.

XX New integrin-targeting transfection complex including lipid - used  
PT to improve transfection efficiency for a very wide range of cells,  
PT useful in, e.g. antisense therapy and genetic immunisation

PS Claim 12; Page 50; 70pp; English.

XX The invention relates to an integrin-targeting transfection complex. The  
CC complex comprises a nucleic acid, an integrin-binding component, a  
CC polycationic nucleic acid-binding component and a lipid. The complexes  
CC are used for in vivo or in vitro transfection of cells, specifically:  
CC (i) for treatment or prevention of disease (in humans or other animals)  
CC caused by defective or deficient genes; (ii) for immunisation; (iii) for  
CC antisense therapy, and (iv) for protein production in host cells, e.g.  
CC of enzymes, therapeutic agents, vaccinating immunogens and diagnostic  
CC antigens. Typical of the diseases that can be treated or prevented are  
CC cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency  
CC virus), cardiovascular disease (e.g. restenosis), leukaemia, asthma and  
CC glaucoma. Incorporation of the lipid into the complex increases  
CC transfection levels from 1-10 percent to over 50 percent. This effect is  
CC observed with all cell types tested including those that are resistant to  
CC transfection by most plasmid vectors. The complexes can carry large  
CC genes, up to 125 kb, e.g. an artificial chromosome. The present sequence  
CC represents a claimed example of an integrin-binding peptide used in the  
CC transfection complexes.

XX Sequence 25 AA;

Query Match

Best Local Similarity 100.0%; Score 57; DB 20; Length 25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9



```

Db          3 crretawac 11
|||||
RESULT 10
R76195
ID R76195 standard; peptide; 9 AA.
XX
AC R76195;
XX
DT 24-JAN-1996 (first entry)
XX
DE Alpha5/betal integrin binding peptide #6.
XX
KW High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;
KW alphav/beta3; RGD; stable configuration; wound healing; tumour;
KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
KW smooth muscle cell migration.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 3 /note= "Any amino acid, esp. Arg, Lys, Gly, Phe,
FT Glu, Asp, Ala, Ser or His"
FT
FT Misc-difference 6 /note= "Any amino acid, esp. Ala, Glu, Gln, Gly,
FT Leu Ser or Asn"
FT
FT Misc-difference 8 /note= "Any amino acid, esp. Ala, His, Arg, Gln,
FT Trp, Gly, Met or Ser"
FT
XX WO9514714-A1.
XX
PD 01-JUN-1995.
XX
PF 22-NOV-1994; 94WO-US13542.
XX
PR 04-AUG-1994; 94US-0286861.
PR 24-NOV-1993; 93US-0158001.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Koivunen E, Ruoslahti E;
XX
DR WPI; 1995-206899/27.
XX
PT High affinity integrin binding peptides - can be used to attach
PT cells to a substrate, inhibit the attachment of osteoclasts to bone,
PT promote wound healing, inhibit angiogenesis, metastasis of tumours
PT and migration of smooth muscle cells
XX
PS Claim 8; Page 60; 86pp; English.
XX
CC The sequences given in R76185-200 and R79073-94 are high affinity
CC integrin binding peptides which bind to various integrins. Peptides
CC which bind to alpha5/betal integrins contain the motifs given in
CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3
CC integrins contain the motif given in R76187. Alphav/beta5 integrins
CC are also bound by RGD containing peptides. These peptides assume a
CC conformationally stabilised configuration which is due to the
CC formation of a disulphide bond, a peptide bond or a lactam bond.
CC These peptides may be used for isolating the complementary integrin
CC from a sample mixture by contacting them under ionic conditions to
CC allow binding of the integrin to the peptide and then separating the
CC integrin from the peptide. They can be used for attaching cells to
CC a substrate, by binding them to the substrate with the cell...the
CC peptides promote wound healing when applied locally and inhibit the
CC attachment of osteoclasts to bone. They inhibit angiogenesis,
CC metastasis of tumours and migration of smooth muscle cells.
XX
SQ Sequence 9 AA;

Query Match 75.4%; Score 43; DB 16; Length 9;
Best Local Similarity 66.7%; Pred No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 crxetxwc 9

RESULT 11
R79082
ID R79082 standard; peptide; 10 AA.
XX
AC R79082;
XX
DT 24-JAN-1996 (first entry)
XX
DE Alpha5/betal integrin binding peptide #12.
XX
KW High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;
KW alphav/beta3; RGD; stable configuration; wound healing;
KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
KW smooth muscle cell migration.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Any amino acid"
FT Misc-difference 4 /note= "Any amino acid"
FT Misc-difference 7 /note= "Any amino acid"
FT Misc-difference 9 /note= "Any amino acid"
FT
XX WO9514714-A1.
XX
PD 01-JUN-1995.
XX
PF 22-NOV-1994; 94WO-US13542.
XX
PR 04-AUG-1994; 94US-0286861.
PR 24-NOV-1993; 93US-0158001.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Koivunen E, Ruoslahti E;
XX
DR WPI; 1995-206899/27.
XX
PT High affinity integrin binding peptides - can be used to attach
PT cells to a substrate, inhibit the attachment of osteoclasts to bone,
PT promote wound healing, inhibit angiogenesis, metastasis of tumours
PT and migration of smooth muscle cells
XX
PS Example 8; Page 33; 86pp; English.
XX
CC The sequences given in R76185-200 and R79073-94 are high affinity
CC integrin binding peptides which bind to various integrins. Peptides
CC which bind to alpha5/betal integrins contain the motifs given in
CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3
CC integrins contain the motif given in R76187. Alphav/beta5 integrins
CC are also bound by RGD containing peptides. These peptides assume a
CC conformationally stabilised configuration which is due to the
CC formation of a disulphide bond, a peptide bond or a lactam bond.
CC These peptides may be used for isolating the complementary integrin
CC from a sample mixture by contacting them under ionic conditions to
CC allow binding of the integrin to the peptide and then separating the
CC integrin from the peptide. They can be used for attaching cells to
CC a substrate, by binding them to the substrate with the cell...the
CC peptides promote wound healing when applied locally and inhibit the

```

Tue Feb 27 09:01:23 2001

CC attachment of osteoclasts to bone. They inhibit angiogenesis,  
 CC metastasis of tumours and migration of smooth muscle cells.  
 XX  
 XX  
 SQ

Sequence 10 AA:

Query Match 75.4%; Score 43; DB 16; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 0.41;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
 II III I  
 DB 2 crxtxwxc 10

## RESULT 12

ID R79081 standard; peptide; 9 AA.

XX AC R79081;

DT 24-JAN-1996 (first entry)

XX Alpha5/beta1 integrin binding peptide #11.

DE High affinity; integrin binding peptide; alpha5/beta1; alphav/beta5;  
 XX alphav/beta3; RGD; stable configuration; wound healing;  
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;  
 KW smooth muscle cell migration.

XX Synthetic.

XX OS WO9514714-A1.

XX PN 01-JUN-1995.

XX PD 22-NOV-1994; 94WO-US13542.

XX PF 04-AUG-1994; 94US-0286861.

XX PR 24-NOV-1993; 93US-0158001.

XX PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX PI Koivunen E, Ruoslahti E;

XX XX WPI: 1995-206899/27.

XX High affinity integrin binding peptides - can be used to attach  
 PT cells to a substrate, inhibit the attachment of osteoclasts to bone,  
 PT promote wound healing, inhibit angiogenesis, metastasis of tumours  
 PT and migration of smooth muscle cells

XX Example 8; Page 33; 86pp; English.

XX The sequences given in R76185-200 and R79073-94 are high affinity  
 CC integrin binding peptides which bind to various integrins. Peptides  
 CC which bind to alpha5/beta1 integrins contain the motifs given in  
 CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3  
 CC integrins contain the motif given in R76187. Alphav/beta5 integrins  
 CC are also bound by RGD containing peptides. These peptides assume a  
 CC conformationally stabilised configuration which is due to the  
 CC formation of a disulphide bond, a peptide bond or a lactam bond.  
 CC These peptides may be used for isolating the complementary integrin  
 CC from a sample mixture by contacting them under ionic conditions to  
 CC allow binding of the integrin to the peptide and then separating the  
 CC integrin from the peptide. They can be used for attaching cells to  
 CC a substrate, by binding them to the substrate with the cell. The  
 CC peptides promote wound healing when applied locally and inhibit the  
 CC attachment of osteoclasts to bone. They inhibit angiogenesis,  
 CC metastasis of tumours and migration of smooth muscle cells.

XX Sequence 9 AA;

SQ

Query Match 70.2%; Score 40; DB 16; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+05;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
 II III I  
 DB 1 crsetywc 9

## RESULT 13

ID Y29195 standard; Protein; 170 AA.

XX AC Y29195;

XX DT 25-OCT-1999 (first entry)

XX Amino acid sequence of a virulence factor encoded by ORF26762c.

XX Human pathogen; virulence polypeptide; virulence factor;  
 KW pathogenic infection; Pseudomonas aeruginosa infection.

XX OS Pseudomonas aeruginosa.

XX PN WO9927129-A1.

XX PD 03-JUN-1999.

XX PF 25-NOV-1998; 98WO-US25247.

XX PR 25-NOV-1997; 97US-0066517.

XX PA (GEHO) GEN HOSPITAL CORP.

XX Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;

XX PI Rahme LG, Tan M, Tsongalis J;

XX XX WPI: 1999-357851/30.

XX Virulence factors useful in developing disease treatments

XX Disclosure; Fig 4; 228pp; English.

XX The present sequence represents a Pseudomonas aeruginosa polypeptide  
 CC sequence. P. aeruginosa is an opportunistic human pathogen present in  
 CC soil water and plants. The specification describes virulence polypeptides  
 CC and nucleic acid sequence encoding such polypeptides. These sequences  
 CC can be used to identify a compound which is capable of decreasing the  
 CC expression of a pathogenic virulence factor. Compounds that inhibit  
 CC the expression or activity of virulence factor polypeptides can be  
 CC used to treat pathogenic infections, especially where the infection  
 CC is a P. aeruginosa infection.  
 CC note: the sequences given in the specification were poorly legible, and  
 CC in some instances assumptions were made as to the identity of the  
 CC residue; it is therefore possible that the sequence given below is  
 CC not entirely correct.

XX Sequence 170 AA;

Query Match 70.2%; Score 40; DB 20; Length 170;

Best Local Similarity 87.5%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRETAWAC 9

DB 34 rrwawac 41

## RESULT 14

ID R76198 standard; peptide; 7 AA.

XX R76198;  
 XX  
 DT 24-JAN-1996 (first entry)  
 XX  
 DE Alpha5/betal integrin binding peptide #9.  
 XX  
 KW High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;  
 KW alphav/beta3; RGD; stable configuration; wound healing;  
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;  
 KW smooth muscle cell migration.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9514714-A1.  
 XX  
 PD 01-JUN-1995.  
 XX  
 PF 22-NOV-1994; 94WO-US13542.  
 XX  
 PR 04-AUG-1994; 94US-0286861.  
 PR 24-NOV-1993; 93US-0158001.  
 XX  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 PI Koivunen E, Ruoslahti E;  
 XX  
 DR WPI; 1995-206899/27.  
 XX  
 PT High affinity integrin binding peptides - can be used to attach  
 PT cells to a substrate, inhibit the attachment of osteoclasts to bone,  
 PT promote wound healing, inhibit angiogenesis, metastasis of tumours  
 PT and migration of smooth muscle cells  
 XX  
 PS Disclosure; Page 8; 86pp; English.  
 XX  
 CC The sequences given in R76185-200 and R79073-94 are high affinity  
 CC integrin binding peptides which bind to various integrins. Peptides  
 CC which bind to alpha5/betal integrins contain the motifs given in  
 CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3  
 CC integrins contain the motif given in R76187. Alphav/beta5 integrins  
 CC are also bound by RGD containing peptides. These peptides assume a  
 CC conformationally stabilised configuration which is due to the  
 CC formation of a disulphide bond, a peptide bond or a lactam bond.  
 CC These peptides may be used for isolating the complementary integrin  
 CC from a sample mixture by contacting them under ionic conditions to  
 CC allow binding of the integrin to the peptide and then separating the  
 CC integrin from the peptide. They can be used for attaching cells to  
 CC a substrate, by binding them to the substrate with the cell. The  
 CC peptides promote wound healing when applied locally and inhibit the  
 CC attachment of osteoclasts to bone. They inhibit angiogenesis,  
 CC metastasis of tumours and migration of smooth muscle cells.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 68.4%; Score 39; DB 16; Length 7;  
 Best Local Similarity 100.0%; Pred. NO. 2.1e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 RRETAWA 8  
 |||||  
 Db 1 rretawa 7  
 RESULT 15  
 R76192  
 ID R76192 standard; peptide; 7 AA.  
 XX  
 AC R76192;  
 XX  
 DT 24-JAN-1996 (first entry)  
 XX

DE Alpha5/betal integrin binding peptide #4.  
 XX  
 KW High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;  
 KW alphav/beta3; RGD; stable configuration; wound healing;  
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;  
 KW smooth muscle cell migration.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9514714-A1.  
 XX  
 PD 01-JUN-1995.  
 XX  
 PF 22-NOV-1994; 94WO-US13542.  
 XX  
 PR 04-AUG-1994; 94US-0286861.  
 PR 24-NOV-1993; 93US-0158001.  
 XX  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 PI Koivunen E, Ruoslahti E;  
 XX  
 DR WPI; 1995-206899/27.  
 XX  
 PT High affinity integrin binding peptides - can be used to attach  
 PT cells to a substrate, inhibit the attachment of osteoclasts to bone,  
 PT promote wound healing, inhibit angiogenesis, metastasis of tumours  
 PT and migration of smooth muscle cells  
 XX  
 PS Claim 5; Page 60; 86pp; English.  
 XX  
 CC The sequences given in R76185-200 and R79073-94 are high affinity  
 CC integrin binding peptides which bind to various integrins. Peptides  
 CC which bind to alpha5/betal integrins contain the motifs given in  
 CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3  
 CC integrins contain the motif given in R76187. Alphav/beta5 integrins  
 CC are also bound by RGD containing peptides. These peptides assume a  
 CC conformationally stabilised configuration which is due to the  
 CC formation of a disulphide bond, a peptide bond or a lactam bond.  
 CC These peptides may be used for isolating the complementary integrin  
 CC from a sample mixture by contacting them under ionic conditions to  
 CC allow binding of the integrin to the peptide and then separating the  
 CC integrin from the peptide. They can be used for attaching cells to  
 CC a substrate, by binding them to the substrate with the cell. The  
 CC peptides promote wound healing when applied locally and inhibit the  
 CC attachment of osteoclasts to bone. They inhibit angiogenesis,  
 CC metastasis of tumours and migration of smooth muscle cells.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 68.4%; Score 39; DB 16; Length 7;  
 Best Local Similarity 100.0%; Pred. NO. 2.1e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 RRETAWA 8  
 |||||  
 Db 1 rretawa 7  
 Search completed: February 27, 2001, 09:00:55  
 Job time: 56 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2001, 09:00:00 ; Search time 42.98 seconds  
(without alignments)  
32.075 Million cell updates/sec

Title: US-09-307-223-1  
Perfect score: 57  
Sequence: 1 CRRETAWAC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 954730 seqs, 153174147 residues

Total number of hits satisfying chosen parameters: 954730

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA:\*

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- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep.\*
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- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*
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- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
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- 25: /cgn2\_6/ptodata/2/paa/US101\_COMB.pep.\*
- 26: /cgn2\_6/ptodata/2/paa/US102\_COMB.pep.\*
- 27: /cgn2\_6/ptodata/2/paa/US103\_COMB.pep.\*
- 28: /cgn2\_6/ptodata/2/paa/US104\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	9	1	PCT-US94-13542-12
2	57	100.0	9	16	US-09-228-901-18
3	57	100.0	9	17	US-09-307-223-1
4	57	100.0	9	17	US-09-364-597A-12
5	57	100.0	9	18	US-09-424-656-13

Sequence 6, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 63, Appl  
Sequence 35, Appl  
Sequence 16, Appl  
Sequence 23046, A  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 18709, A  
Sequence 163, App  
Sequence 26215, A  
Sequence 43165, A  
Sequence 25, Appl  
Sequence 25, Appl  
Sequence 299, App  
Sequence 299, App  
Sequence 299, App  
Sequence 299, App  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 241, App  
Sequence 240, App  
Sequence 32565, A  
Sequence 3053, A  
Sequence 3067, App  
Sequence 19138, A  
Sequence 697, App  
Sequence 29287, A  
Sequence 20057, A  
Sequence 29707, A  
Sequence 33, Appl  
Sequence 25510, A  
Sequence 328, App  
Sequence 351, App

ALIGNMENTS

RESULT 1  
PCT-US94-13542-12  
; Sequence 12, Application PC/TUS9413542  
; GENERAL INFORMATION:  
; APPLICANT: La Jolla Cancer Research Foundation  
; TITLE OF INVENTION: Novel Integrin-Binding Peptides  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/13542  
; FILING DATE: 22-NOV-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/158,001  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hook, Gregory

REGISTRATION NUMBER: 38,701  
REFERENCE/DOCKET NUMBER: FP-LA 1220  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
PCT-US94-13542-12

Query Match 100.0%; Score 57; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.2e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
|||||  
DB 1 CRRETAWAC 9

RESULT 2  
US-09-228-901-18  
; Sequence 18, Application US/09228901  
; GENERAL INFORMATION:  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and  
; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronectin  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/228,901  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/717,169  
; FILING DATE: 20-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2017  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-228-901-18

Query Match 100.0%; Score 57; DB 16; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.2e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
|||||

DB 1 CRRETAWAC 9

RESULT 3  
US-09-307-223-1  
; Sequence 1, Application US/09307223  
; GENERAL INFORMATION:  
; APPLICANT: VARNER, JUDITH A.  
; TITLE OF INVENTION: METHODS FOR DETECTING AND INHIBITING ANGIOGENESIS  
; FILE REFERENCE: 6627VARNPALL  
; CURRENT APPLICATION NUMBER: US/09/307,223  
; CURRENT FILING DATE: 1999-05-07  
; EARLIER APPLICATION NUMBER: 60/084,850  
; EARLIER FILING DATE: 1998-05-08  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE  
US-09-307-223-1

Query Match 100.0%; Score 57; DB 17; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.2e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
|||||  
DB 1 CRRETAWAC 9

RESULT 4  
US-09-364-597A-12  
; Sequence 12, Application US/09364597A  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Koivunen, Erkki  
; TITLE OF INVENTION: Novel Integrin-Binding Peptides  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/364,597A  
; FILING DATE: 30-JUL-1999  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/158,001  
; FILING DATE: 24-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,861  
; FILING DATE: 04-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 3419  
; TELEPHONE: (858) 535-9001  
; TELEFAX: (858) 535-8949  
; INFORMATION FOR SEQ ID NO: 12:

```
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 9 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: circular
US-09-364-597A-12

Query Match 100.0%; Score 57; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 5
US-09-424-656-13
; Sequence 13, Application US/09424656
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-424-656-13

Query Match 100.0%; Score 57; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 6
US-60-208-451-6
; Sequence 6, Application US/60208451
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J
; APPLICANT: Kovesdi, Imre
; APPLICANT: Roelvink, Petrus W
; APPLICANT: Einfeld, David
; APPLICANT: Brough, Douglas E
; APPLICANT: Lizonova, Alena
; TITLE OF INVENTION: ALTERNATIVELY TARGETED ADENOVIRUS
; FILE REFERENCE: 205046
; CURRENT APPLICATION NUMBER: US/60/208,451
; CURRENT FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT

; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 9 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: circular
US-09-364-597A-12

Query Match 100.0%; Score 57; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 5
US-09-424-656-13
; Sequence 13, Application US/09424656
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-424-656-13

Query Match 100.0%; Score 57; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 6
US-60-208-451-6
; Sequence 6, Application US/60208451
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J
; APPLICANT: Kovesdi, Imre
; APPLICANT: Roelvink, Petrus W
; APPLICANT: Einfeld, David
; APPLICANT: Brough, Douglas E
; APPLICANT: Lizonova, Alena
; TITLE OF INVENTION: ALTERNATIVELY TARGETED ADENOVIRUS
; FILE REFERENCE: 205046
; CURRENT APPLICATION NUMBER: US/60/208,451
; CURRENT FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT

; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 12 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: circular
US-09-424-656-11

Query Match 100.0%; Score 57; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 7
US-09-424-656-11
; Sequence 11, Application US/09424656
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-424-656-11

Query Match 100.0%; Score 57; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 3 CRRETAWAC 11

RESULT 8
US-09-424-656-12
; Sequence 12, Application US/09424656
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
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TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-424-656-12

Query Match 100.0%; Score 57; DB 18; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9  
Db 3 CRRETAWAC 11

RESULT 9  
PCT-US94-13542-6  
; Sequence 6, Application PC/TUS9413542  
; GENERAL INFORMATION:  
; APPLICANT: La Jolla Cancer Research Foundation  
; TITLE OF INVENTION: Novel Integrin-Binding Peptides  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/13542  
; FILING DATE: 22-NOV-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/158,001  
; FILING DATE: 24-NOV-1993  
; NAME: Hook, Gregory  
; REGISTRATION NUMBER: 38,701  
; REFERENCE/DOCKET NUMBER: FP-LA 1220  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: circular  
PCT-US94-13542-6

Query Match 100.0%; Score 57; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9  
Db 3 CRRETAWAC 11

RESULT 10  
US-09-364-597A-6  
; Sequence 6, Application US/09364597A  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Koivunen, Erkki  
; TITLE OF INVENTION: Novel Integrin-Binding Peptides

NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/364,597A  
FILING DATE: 30-JUL-1999  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/158,001  
FILING DATE: 24-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,861  
FILING DATE: 04-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 3419  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (858) 535-9001  
TELEFAX: (858) 535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
US-09-364-597A-6

Query Match 100.0%; Score 57; DB 17; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9  
Db 3 CRRETAWAC 11

RESULT 11  
US-09-406-781-63  
; Sequence 63, Application US/09406781  
; GENERAL INFORMATION:  
; APPLICANT: Kenten, John  
; APPLICANT: Roberts, Steven  
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS  
; FILE REFERENCE: 2757-3  
; CURRENT APPLICATION NUMBER: US/09/406,781  
; CURRENT FILING DATE: 1999-09-28  
; EARLIER APPLICATION NUMBER: 60/119,851  
; EARLIER FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 63  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: binding peptide  
US-09-406-781-63

Query Match 100.0%; Score 57; DB 18; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-307-223-1.rap

Tue Feb 27 09:01:24 2001

APPLICATION NUMBER: US/09/424,656

FILING DATE:

PRIOR APPLICATION DATA: GB 9711115.7

APPLICATION NUMBER: GB 9711115.7

FILING DATE: 29-MAY-1997

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: circular

MOLECULE TYPE: peptide

US-09-424-656-16

Query Match 100.0%; Score 57; DB 18; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9

Db 3 CRRETAWAC 11

RESULT 14

US-09-252-991A-23046

Sequence 23046, Application US/09252991A

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23046

LENGTH: 196

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23046

Query Match 78.9%; Score 45; DB 16; Length 196;

Best Local Similarity 77.8%; Pred. No. 8.3;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9

Db 118 CRRETAWAC 126

RESULT 15

PCT-US94-13542-11

Sequence 11, Application PC/TUS9413542

GENERAL INFORMATION:

APPLICANT: La Jolla Cancer Research Foundation

TITLE OF INVENTION: Novel Integrin-Binding Peptides

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

1 CRRETAWAC 9

111111111

3 CRRETAWAC 11

RESULT 12

S-09-455-061-35

Sequence 35, Application US/09455061

GENERAL INFORMATION:

APPLICANT: Wickham, Thomas J.

APPLICANT: Roelink, Petrus W.

APPLICANT: Kovesdi, Imre

TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF

TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Volt &amp; Mayer, Ltd.

STREET: Two Prudential Plaza - 49th Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/455,061

FILING DATE: 06-DEC-1999

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 9-130225

FILING DATE: 06-AUG-1998

PRIOR APPLICATION NUMBER: US 8-701124

FILING DATE: 21-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hefner, M. Daniel

REGISTRATION NUMBER: 41,826

REFERENCE/DOCKET NUMBER: 203128

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-455-061-35

Query Match 100.0%; Score 57; DB 18; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0089;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9

Db 3 CRRETAWAC 11

RESULT 13

US-09-424-656-16

Sequence 16, Application US/09424656

GENERAL INFORMATION:

APPLICANT: INTEGRIN-TARGETING VECTORS HAVING

TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY

NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:



SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13542  
FILING DATE: 22-NOV-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/158,001  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hook, Gregory  
REGISTRATION NUMBER: 38,701  
REFERENCE/DOCKET NUMBER: FP-LA 1220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
PCT-US94-13542-11

Query Match 75.4%; Score 43; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 8.2e+05;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CRRETAWAC 9  
Db 1 CRXETWXC 9

Search completed: February 27, 2001, 09:02:06  
Job time: 126 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 27, 2001, 09:00:00 ; Search time 14.18 seconds  
(without alignments)  
43.096 Million cell updates/sec

Title: US-09-307-223-1

Perfect score: 57

Sequence: 1 CRRETAWAC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

PIR\_66: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	71.9	263	1 S43189	hypothetical prote
2	38	66.7	272	2 T23633	hypothetical prote
3	38	66.7	500	2 T50868	exopolysphatase
4	37	64.9	269	2 G81230	conserved hypothet
5	37	64.9	269	2 D82001	probable integral
6	37	64.9	307	2 D70741	hypothetical prote
7	36	63.2	233	2 H72648	hypothetical prote
8	36	63.2	300	2 A60956	dyein beta heavy
9	36	63.2	323	2 T24372	hypothetical prote
10	36	63.2	334	2 T17213	hypothetical prote
11	36	63.2	465	2 T24419	hypothetical prote
12	36	63.2	535	2 S66148	gene pipsqueak pro
13	36	63.2	2055	2 T00093	hypothetical prote
14	35	61.4	87	2 S36319	T-cell receptor de
15	35	61.4	131	2 S36301	T-cell receptor de
16	35	61.4	136	2 S36320	T-cell receptor de
17	35	61.4	137	2 S36311	T-cell receptor de
18	35	61.4	141	2 S36318	T-cell receptor de
19	35	61.4	142	2 S36316	T-cell receptor de
20	35	61.4	143	2 S36310	T-cell receptor de
21	35	61.4	145	2 S36309	T-cell receptor de
22	35	61.4	265	2 S76808	hypothetical prote
23	35	61.4	284	1 LNRTL	hepatic lectin - r
24	35	61.4	284	2 S29855	asialoglycoprotein
25	35	61.4	347	2 S11223	UDPglucose 4-epime
26	35	61.4	392	1 RWHUPD	poliovirus recepto
27	35	61.4	417	1 RWHUPA	poliovirus recepto
28	35	61.4	417	1 RWHUPA	poliovirus recepto
29	35	61.4	530	2 JC6030	3-oxo-5alpha-ster

30 35 61.4 661 2 T48943 hypothetical prote  
31 35 61.4 1153 2 T21386 hypothetical prote  
32 34 59.6 102 4 JC5161 hypothetical Orf5  
33 34 59.6 119 2 T17032 fimbriata-associat  
34 34 59.6 137 2 I46628 rearranged T-cell  
35 34 59.6 139 2 I46630 rearranged T-cell  
36 34 59.6 142 2 S36307 T-cell receptor de  
37 34 59.6 143 2 S36321 T-cell receptor de  
38 34 59.6 144 2 S36322 T-cell receptor de  
39 34 59.6 145 2 I46629 rearranged T-cell  
40 34 59.6 145 2 I46631 rearranged T-cell  
41 34 59.6 149 2 S36317 T-cell receptor de  
42 34 59.6 151 2 I46626 rearranged T-cell  
43 34 59.6 151 2 T16284 hypothetical prote  
44 34 59.6 155 2 S76397 hypothetical prote  
45 34 59.6 400 2 E71338 probable ribose/ga

ALIGNMENTS

RESULT 1

S43189

hypothetical protein - Pseudomonas aeruginosa

C:Species: Pseudomonas aeruginosa

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S43189

R:Strich, U.; Wohlfarth, S.; Winkler, U.K.

submitted to the EMBL Data Library, April 1992

A:Reference number: S43188

A:Accession: S43189

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-263 <STR>

A:Cross-references: EMBL:X65613; NID:g469099; PIDN:CAA46565.1; PID:g469101

C:Superfamily: methanol dehydrogenase regulatory protein

Query Match 71.9%; Score 41; DB 1; Length 263;

Best Local Similarity 66.7%; Pred. No. 3.3;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9

Db 240 CRRVAVWRC 248

RESULT 2

T23633

hypothetical protein LLC1.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T23633

R:Matthews, L.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19775

A:Accession: T23633

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-272 <WIL>

A:Cross-references: EMBL:Z82277; PIDN:CAB05250.1; GSPDB:GN00022; CESP:LLC1.2

A:Experimental source: clone LLC1

C:Genetics:

A:Gene: CESP:LLC1.2

A:Map position: 4

A:Introns: 8/1; 81/2; 110/3; 132/1; 172/2; 222/1

Query Match 66.7%; Score 38; DB 2; Length 272;

Best Local Similarity 61.5%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 CRRE----TAWAC 9

```

|||||
Db 190 CRREAGVATWAC 202

RESULT 3
T50868
exopolyphosphatase [imported] - Rubrivivax gelatinosus
C:Species: Rubrivivax gelatinosus
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 18-Aug-2000
C:Accession: T50868
R:Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.
submitted to the EMBL Data Library, November 1999
A:Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosyn
A:Reference number: 225270
A:Accession: T50868
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-500 <NAG>
A:Cross-references: EMBL:AB034704; PIDN:BAA94021.1
A:Experimental source: strain IL144
C:Genetics:
A:Gene: ppx
C:Superfamily: exopolyphosphatase

Query Match 66.7%; Score 38; DB 2; Length 500;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RRETAWAC 9
||| |||
Db 360 RRELGWAC 367

RESULT 4
G81230
conserved hypothetical protein NMB0175 [imported] - Neisseria meningitidis (group B stra
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: G81230
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.;
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: G81230
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-269 <TET>
A:Cross-references: GB:AE002374; GB:AE002098; NID:g7225382; PIDN:AAF40632.1; PID:g722539
A:Experimental source: serogroup B, strain MMD58
C:Genetics:
A:Gene: NMB0175

Query Match 64.9%; Score 37; DB 2; Length 269;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRETAWAC 9
||| |||
Db 193 RKKTWAC 190

RESULT 5
D82001
probable integral membrane protein NMA0093 [imported] - Neisseria meningitidis (group A
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C:Accession: D82001
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:20222556
A:Accession: D82001
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-269 <PAR>
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83409.1; PID:g7377
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0093

Query Match 64.9%; Score 37; DB 2; Length 269;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRETAWAC 9
||| |||
Db 183 RKKTWAC 190

RESULT 6
D70741
hypothetical protein Rv137c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: D70741
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987
A:Accession: D70741
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-307 <COL>
A:Cross-references: GB:Z75555; GB:AL123456; NID:g3261608; PIDN:CAA99962.1; PID:e25055
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv137c

Query Match 64.9%; Score 37; DB 2; Length 307;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
||| |||
Db 5 CORATAFAC 13

RESULT 7
H72648
hypothetical protein AP50622 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: H72648
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:99310339
A:Accession: H72648
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <KAW>
A:Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79592.1; PID:d1043378; PID:9
A:Experimental source: strain K1
C:Genetics:

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A:Gene: APE0622

Query Match 63.2%; Score 36; DB 2; Length 233;  
Best Local Similarity 55.6%; Pred. No. 24;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
I: ||||  
Db 164 CQAPAAWAC 172

RESULT 8

A60956  
dynein beta heavy chain, ciliary - sea urchin (Strongylocentrotus purpuratus) (fragment)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 11-Jan-2000  
C:Accession: A60956  
R:Fortz, K.R.; Asai, D.J.  
Cell Motil. Cytoskeleton 16, 33-46, 1990  
A:Title: Molecular cloning and expression of sea urchin embryonic ciliary dynein beta he

A:Reference number: A60956; MUID:90284040.

A:Accession: A60956

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-300 <FOL>

C:Superfamily: Escherichia citrate (pro-3S)-lyase alpha chain

Query Match 63.2%; Score 36; DB 2; Length 300;  
Best Local Similarity 66.7%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
I: ||||  
Db 4 CQDTRAKAC 12

RESULT 9

T24372  
hypothetical protein T02G6.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T24372  
R:McLay, K.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19883

A:Accession: T24372

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-323 <WIL>

A:Cross-references: EMBL:Z81583; PIDN:CAB04669.1; GSPDB:GN00019; CESP:T02G6.4

A:Experimental source: clone T02G6

C:Genetics:

A:Gene: CESP:T02G6.4

A:Map position: 1

A:Introns: 96/1; 144/2; 177/1; 203/3; 224/2; 237/3; 255/2; 286/1; 312/2

C:Superfamily: Caenorhabditis elegans hypothetical protein T02G6.4

Query Match 63.2%; Score 36; DB 2; Length 323;  
Best Local Similarity 44.4%; Pred. No. 32;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
I: || : ||  
Db 272 CORRSWAC 280

RESULT 10

T17213  
hypothetical protein DKFZp434E0335.1 - human (fragment)  
C:Species: Homo sapiens (man)

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T17213  
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, September 1999  
A:Reference number: Z18723

A:Accession: T17213

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-334 <POU>

A:Cross-references: EMBL:AL117402

A:Experimental source: adult testis; clone DKFZp434E0335

C:Genetics:

A:Note: DKFZp434E0335.1

Query Match 63.2%; Score 36; DB 2; Length 334;  
Best Local Similarity 71.4%; Pred. No. 33;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAW 7  
I: || : ||  
Db 175 CRDITLM 181

RESULT 11

T24419

hypothetical protein T04A11.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jul-2000

C:Accession: T24419

R:Barlow, K.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19888

A:Accession: T24419

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-465 <WIL>

A:Cross-references: EMBL:Z83123; PIDN:CAB05613.1; GSPDB:GN00022; CESP:T04A11.10

A:Experimental source: clone T04A11

C:Genetics:

A:Gene: CESP:T04A11.10

A:Map position: 4

A:Introns: 78/3; 148/3; 232/3; 270/2; 368/1

C:Superfamily: Caenorhabditis elegans hypothetical protein C33A12.9b

Query Match 63.2%; Score 36; DB 2; Length 465;  
Best Local Similarity 44.4%; Pred. No. 44;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
I: || : ||  
Db 454 CKRRCSTWC 462

RESULT 12

S66148

gene pipsqueak protein A short form - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jul-2000

C:Accession: S66148

R:Weber, U.; Siegel, V.; Mlodzik, M.

EMBO J. 14, 6247-6257, 1995

A:Title: pipsqueak encodes a novel nuclear protein required downstream of seven-up fo

A:Reference number: S66148; MUID:96134923

A:Accession: S66148

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-535 <WEB>

A:Cross-references: EMBL:X90986; NID:g1149498; PIDN:CAAG2473.1; PID:g1149499

C:Genetics:

A:Gene: pipsqueak

C:Superfamily: POZ domain homology

F:21-123/Domain: POZ domain homology <POZ>

Query Match 63.2%; Score 36; DB 2; Length 535;

Best Local Similarity 55.6%; Pred. No.: 49;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9

|||

Db 481 CRTAACWAC 489

RESULT 13

T00093

Hypothetical protein KIAA0467 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 21-Jul-2000

C:Accession: T00093

R:Seiki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, D.; Nakajima, N.;

DNA Res. 4; 345-349, 1997

A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human

A:Reference number: Z14085; MUID:98116662

A:Accession: T00093

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2055 <SEK>

A:Cross-references: EMBL:AB007936; NID:g3413895; PIDN:BAA32312.1; PID:g3413896

A:Experimental source: brain

C:Genetics:

A:Map position: 1

A:Note: KIAA0467

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 2055;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAW 7

|||

Db 1855 CRDRTLW 1861

RESULT 14

S36319

T-cell receptor delta chain precursor - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999

C:Accession: S36319; S23034

R:Hein, W.R.; Dudley, L.

EMBO J. 12, 715-724, 1993

A:Title: Divergent evolution of T cell repertoires: extensive diversity and developmenta

A:Reference number: S36287; MUID:93178447

A:Accession: S36319

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-87 <HEI>

A:Cross-references: EMBL:212991; NID:g2246; PIDN:CAA78335.1; PID:g2247

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 61.4%; Score 35; DB 2; Length 87;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWA 8

|||

Db 43 CRYETWS 50

RESULT 15

S36301

T-cell receptor delta chain - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999

C:Accession: S36301; S22985

R:Hein, W.R.; Dudley, L.

EMBO J. 12, 715-724, 1993

A:Title: Divergent evolution of T cell repertoires: extensive diversity and developme

A:Reference number: S36287; MUID:93178447

A:Accession: S36301

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <HEI>

A:Cross-references: EMBL:212973; NID:g2211; PIDN:CAA78317.1; PID:g2212

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 61.4%; Score 35; DB 2; Length 131;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWA 8

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Db 43 CRYETWS 50

Search completed: February 27, 2001, 09:00:36

Job time: 36 sec

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Sequence 5,	Appli
Sequence 5,	Appli
Sequence 24,	Appli
Sequence 25,	Appli
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Sequence 5,	Appli
Sequence 36,	Appli
Sequence 4,	Appli
Sequence 36,	Appli
Sequence 36,	Appli
Sequence 4,	Appli

## ALIGNMENTS

```

RESULT      1
US-08-425-238-6
; Sequence 6, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,238

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FILING DATE: 514  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER: US 08/158,001  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 9775  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-425-238-6

Query Match	100.0%	Score 57; DB 1; Length 9;
Best Local Similarity	100.0%;	Pred. No. 1.3e+05;
Matches	9. Conservative	Mismatches 0; Indels

Qy 1 CRRETAWAC 9  
| | | | | | | |  
Db 1 CRRETAWAC 9

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 27, 2001, 08:59:59 ; Search time 12.5 Seconds  
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12.929 Million cell updates

US-09-307-223-1

Title:	57
perfect score:	1
Sequence:	CRRETAWAC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

searched: 174772 seqs, 17957048 residues

Total number of bits satisfying chosen parameters: 174772

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Minimum DB* seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 s

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5: /cgn2_6/ptodata/2/1aa/backfiles1.pcp.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		ID	Description
		Match	Length		
1	57	100.0	9	US-08-425-238-6	Sequence 6, Appl
2	57	100.0	9	US-08-717-169-18	Sequence 18, Appl
3	57	100.0	9	US-08-286-861-12	Sequence 12, Appl
4	57	100.0	13	US-08-425-238-3	Sequence 3, Appl
5	57	100.0	13	US-08-701-124-35	Sequence 35, Appl
6	57	100.0	13	US-08-286-861-6	Sequence 6, Appl
7	57	100.0	13	US-09-130-225-35	Sequence 35, Appl
8	43	75.4	9	US-08-286-861-11	Sequence 11, Appl
9	43	75.4	10	US-08-286-861-26	Sequence 26, Appl
10	40	70.2	9	US-08-286-861-25	Sequence 25, Appl
11	39	68.4	7	US-08-425-238-5	Sequence 5, Appl
12	39	68.4	7	US-08-286-861-8	Sequence 8, Appl
13	39	68.4	9	US-08-425-238-10	Sequence 10, Appl
14	39	68.4	13	US-08-425-238-11	Sequence 11, Appl
15	35	61.4	14	5514582-14	Patent No. 5514582
16	34	59.6	44	US-09-188-930-296	Sequence 296, App
17	34	59.6	552	US-08-796-899-28	Sequence 28, Appl
18	33	57.9	211	US-08-708-958-2	Sequence 2, Appl
19	32	56.1	108	US-08-560-398-6	Sequence 6, Appl
20	32	56.1	114	5514582-13	Patent No. 5514582
21	32	56.1	114	5514582-14	Patent No. 5514582
22	32	56.1	255	US-08-484-905-110	Sequence 110, App
23	32	56.1	255	US-08-481-985B-110	Sequence 110, App
24	32	56.1	255	US-08-370-476-110	Sequence 110, App
25	32	56.1	539	5198359-4	Patent No. 5198359
26	32	56.1	539	5447566-4	Patent No. 5447566
27	31	54.4	33	US-08-651-136C-30	Sequence 30, Appl
28	31	54.4	222	US-08-651-136C-14	Sequence 14, Appl

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.861
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9992
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-08-286-861-12

Query Match      100.0%; Score 57; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CRRETAWAC 9
Db   1 CRRETAWAC 9

RESULT 4
US-08-425-238-3
; Sequence 3, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NO. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
FILING DATE: 04-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-08-286-861-6

Query Match 100.0%; Score 57; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
DB 3 CRRETAWAC 11

RESULT 7
US-09-130-225-35
; Sequence 35, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-130-225-35

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-286-861-6

Query Match 100.0%; Score 57; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
DB 3 CRRETAWAC 11

RESULT 6
US-08-286-861-6
; Sequence 6, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

```



Query Match 100.0%; Score 57; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRETAWAC 9  
||| ||| ||| |||

Db 3 CRETAWAC 11

## RESULT 8

US-08-286-861-11  
; Sequence 11, Application US/08286861  
; Patent No. 5981478  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Koivunen, Erkki  
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,861  
; FILING DATE: 04-AUG-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/158,001  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 9992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-8949  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: circular

US-08-286-861-11

Query Match 75.4%; Score 43; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRETAWAC 9  
||| ||| |||

Db 1 CRXETXWC 9

## RESULT 9

US-08-286-861-26  
; Sequence 26, Application US/08286861  
; Patent No. 5981478  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Koivunen, Erkki  
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores

; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,861  
; FILING DATE: 04-AUG-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/158,001  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 9992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: both

US-08-286-861-26

Query Match 75.4%; Score 43; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 0.19;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRETAWAC 9  
||| ||| ||| |||

Db 2 CRXETXWC 10

## RESULT 10

US-08-286-861-25  
; Sequence 25, Application US/08286861  
; Patent No. 5981478  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Koivunen, Erkki  
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,861  
; FILING DATE: 04-AUG-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/158,001  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 9992



;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/425,238  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/158,001  
;; FILING DATE: 24-NOV-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LA 9775  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1  
;; OTHER INFORMATION: /note= "Xaa - an amino acid capable  
;; OF FORMING A DISULFIDE BOND."  
;;  
;; NAME/KEY: Peptide  
;; LOCATION: 9  
;; OTHER INFORMATION: /note= "Xaa - an amino acid capable  
;; OF FORMING A DISULFIDE BOND."  
;;  
US-08-425-238-10

Query Match 68.4%; Score 39; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRETAWA 8  
| | | | |  
Db 2 RRETAWA 8

RESULT 14  
US-08-425-238-11  
;; Sequence 11, Application US/08425238  
;; Patent No. 5627263  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruoslahti, Erkki  
;; APPLICANT: Koivinen, Erkki  
;; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Campbell and Flores  
;; STREET: 4370 La Jolla Village Drive, Suite 700  
;; CITY: San Diego  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 92122  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/425,238  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/158,001  
;; FILING DATE: 24-NOV-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815

;; REFERENCE/DOCKET NUMBER: P-LA 9775  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 13 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 3  
;; OTHER INFORMATION: /note= "Xaa - an amino acid capable  
;; OF FORMING A DISULFIDE BOND."  
;;  
;; NAME/KEY: Peptide  
;; LOCATION: 11  
;; OTHER INFORMATION: /note= "Xaa - an amino acid capable  
;; OF FORMING A DISULFIDE BOND."  
;;  
US-08-425-238-11

Query Match 68.4%; Score 39; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRETAWA 8  
| | | | |  
Db 4 RRETAWA 10

RESULT 15  
5514582-10  
;; Patent No. 5514582  
;; APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.  
;; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID  
;; IMMUNOGLOBULINS  
;; NUMBER OF SEQUENCES: 43  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/185,670  
;; FILING DATE: 21-JAN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 986,931  
;; FILING DATE: 08-DEC-1992  
;; APPLICATION NUMBER: 808,122  
;; FILING DATE: 16-DEC-1991  
;; APPLICATION NUMBER: 440,625  
;; FILING DATE: 22-NOV-1989  
;; APPLICATION NUMBER: 315,015  
;; FILING DATE: 23-FEB-1989  
;; SEQ ID NO: 10:  
;; LENGTH: 114  
5514582-10

Query Match 61.4%; Score 35; DB 5; Length 114;  
Best Local Similarity 55.6%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9  
| | | | |  
Db 106 CRPYRWVC 114

Search completed: February 27, 2001, 09:00:18  
Job time: 19 sec

